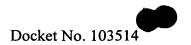


APPENDIX

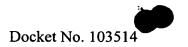
Changes to Claims:

The following are marked-up versions of the amended claims:

- 1. (Amended) Nucleic material, in isolated or purified state, comprising a nucleotide sequence chosen from the group which consists of (i) the sequences SEQ ID NO: 1124, SEQ ID NO: 1146, SEQ ID NO: 1179, SEQ ID NO: 120, SEQ ID NO: 12416, SEQ ID NO: 13021, SEQ ID NO: 14130 and SEQ ID NO: 14231; (ii) the sequences complementary to sequences (i); and (iii) the sequences equivalent to sequences (i) or (ii), in particular the sequences having, for every series of 100 contiguous monomers, at least 50%, and preferentially at least 70% homology with sequences (i) or (ii) respectively.
- 2. (Amended) Nucleic material, in isolated or purified state, encoding a polypeptide having, for every contiguous series of at least 30 amino acids, at least 50%, and preferably at least 70% homology with a peptide sequence chosen from the group which consists of SEQ ID NO: 1135, SEQ ID NO: 1157, SEQ ID NO: 11810, SEQ ID NO: 12113, SEQ ID NO: 13525 and SEQ ID NO: 13726.
- 3. (Amended) Retroviral nucleic material, whose pol gene comprises a nucleotide sequence identical or equivalent to a sequence chosen from the group which consists of SEO ID NO: 1124, SEO ID NO: 12416 and their complementary sequences.
- 4. (Amended) Retroviral nucleic material, in which the 5' end of the pol gene starts at nucleotide 1419 of SEQ ID NO: 13021.
- 5. (Amended) Retroviral nucleic material, in which the pol gene encodes a polypeptide having, for every contiguous series of at least 30 amino acids, at least 50%, and preferably at least 70% homology with the peptide sequence SEQ ID NO: 1135.
- 6. (Amended) Retroviral nucleic material, in which the 3' end of the gag gene ends at nucleotide 1418 of SEQ ID NO: 13021.



- 7. (Amended) Retroviral nucleic material, in which the env gene comprises a nucleotide sequence identical or equivalent to a sequence chosen from the group which consists of SEQ ID NO: 1179, and its complementary sequences.
- 8. (Twice Amended) Retroviral nucleic material, in which the env gene comprises a nucleotide sequence which starts at nucleotide 1 of SEQ ID NO: 1179 and ends at nucleotide 233 of SEQ ID NO: 1146.
- 9. (Amended) Retroviral nucleic material, in which the env gene encodes a polypeptide having, for every contiguous series of at least 30 amino acids, at least 50%, and preferably at least 70% homology with the sequence SEQ ID NO: 11810.
- 10. (Amended) Retroviral nucleic material in which the U3R region of the 3' LTR comprises a nucleotide sequence which ends at nucleotide 617 of SEQ ID NO: 1146.
- 11. (Amended) Retroviral nucleic material in which the RU5 region of the 5'
 LTR comprises a nucleotide sequence which starts at nucleotide 755 of SEQ ID NO: 120 and ends at nucleotide 337 of SEQ ID NO: 14130 or SEQ ID NO: 14231.
- 12. (Amended) Retroviral nucleic material comprising a sequence which starts at nucleotide 755 of SEQ ID NO: 129 and which ends at nucleotide 617 of SEQ ID NO: 1146.
- 14. (Amended) Nucleotide fragment comprising a nucleotide sequence chosen from the group which consists of (i) the sequences SEQ ID NO: 1124, SEQ ID NO: 1146, SEQ ID NO: 11479, SEQ ID NO: 129, SEQ ID NO: 12416, SEQ ID NO: 13021, SEQ ID NO: 14130 and SEQ ID NO: 14231; (ii) the sequences complementary to sequences (i); and (iii) the sequences equivalent to sequences (i) or (ii), in particular the sequences having, for every series of 100 contiguous monomers, at least 50%, and preferentially at least 70% homology with sequences (i) or (ii) respectively.
- 15. (Amended) Nucleotide fragment according to Claim 14, consisting of a nucleotide sequence chosen from the group which consists of (i) the sequences SEQ ID



NO: 1124, SEQ ID NO: 1146, SEQ ID NO: 1179, SEQ ID NO: 120, SEQ ID NO: 12416, SEQ ID NO: 13021, SEQ ID NO: 14130 and SEQ ID NO: 14231; (ii) the sequences complementary to sequences (i); and (iii) the sequences equivalent to sequences (i) or (ii), in particular the sequences having, for every series of 100 contiguous monomers, at least 50%, and preferentially at least 70% homology with sequences (i) or (ii) respectively.

- 16. (Amended) Nucleotide fragment comprising a nucleotide sequence encoding a polypeptide having, for every contiguous series of at least 30 amino acids, at least 50%, and preferably at least 70% homology with a peptide sequence chosen from the group which consists of SEQ ID NO: 1135, SEQ ID NO: 1157, SEQ ID NO: 11810, SEQ ID NO: 12113, SEQ ID NO: 13525 and SEQ ID NO: 13726.
- 17. (Amended) Nucleotide fragment according to claim 16, consisting of a nucleotide sequence encoding a polypeptide having, for every contiguous series of at least 30 amino acids, at least 50%, and preferably at least 70% homology with a peptide sequence chosen from the group which consists of SEQ ID NO: 1135, SEQ ID NO: 1157, SEQ ID NO: 11810, SEQ ID NO: 12113, SEQ ID NO: 13525 and SEQ ID NO: 13726.
- 21. (Amended) Primer according to claim 20, characterized in that its nucleotide sequence is chosen from SEQ ID NO: 1168, SEQ ID NO: 119, SEQ ID NO: 12214, SEQ ID NO: 12315, SEQ ID NO: 12617, SEQ ID NO: 12718, SEQ ID NO: 12819, SEQ ID NO: 12920, SEQ ID NO: 13223, and SEQ ID NO: 13324.
- 24. <u>(Amended)</u> Peptide according to claim 23 comprising a sequence identical, partially or completely, or equivalent to a sequence chosen from SEQ ID NO: 1135, SEQ ID NO: 1157, SEQ ID NO: 11510, SEQ ID NO: 12113, SEQ ID NO: 13525 and SEQ ID NO: 13726.

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